

Amendments

In the Specification:

On page 22, line 27, delete "Bestfit" and insert therefor --Bestfit®--.

On page 23, line 1, delete "Bestfit" and insert therefor --Bestfit®--.

On page 23, line 3, delete "Bestfit" and insert therefor --Bestfit®--.

On page 38, line 16, delete "Bestfit" and insert therefor --Bestfit®--.

On page 38, line 18, delete "Bestfit" and insert therefor --Bestfit®--.

In the Claims:

Please amend the following claims:

Sub E6
D 7 95. An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to amino acids 1 to 260 of SEQ ID NO:42;

wherein % identity is determined using the [Bestfit] Bestfit® program with parameters that calculate % identity over the full length of amino acids 1 to 260 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids 1 to 260 of SEQ ID NO:42.

Sub E1
D 2 98. The isolated polynucleotide of claim 95, wherein said amino acid sequence is at least 95% identical to amino acids 1 to 488 of SEQ ID NO:42;

wherein % identity is determined using the [Bestfit] Bestfit® program with parameters that calculate % identity over the full length of amino acids 1 to 488 of SEQ ID NO:42 and that allow

Sub E7
D2
cont

gaps of up to 5% of the total number of amino acid residues in amino acids 1 to 488 of SEQ ID NO:42.

Sub E8
D3

101. The isolated polynucleotide of claim 98, wherein said amino acid sequence is at least 95% identical to amino acids -17 to 488 of SEQ ID NO:42;

wherein % identity is determined using the [Bestfit] Bestfit[®] program with parameters that calculate % identity over the full length of amino acids -17 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids -17 to 488 of SEQ ID NO:42.

Sub E9
D4

104. The isolated polynucleotide of claim 101, wherein said amino acid sequence is at least 95% identical to amino acids -18 to 488 of SEQ ID NO:42;

wherein % identity is determined using the [Bestfit] Bestfit[®] program with parameters that calculate % identity over the full length of amino acids -18 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids -18 to 488 of SEQ ID NO:42.

Sub E10
D5

115. An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642,

wherein % identity is determined using the [Bestfit] Bestfit[®] program with parameters that calculate % identity over the full length of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of amino

DS
Sub E10
cont
acid residues of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

Sub E11
117. The isolated polynucleotide of claim 115, wherein said amino acid sequence is at least 95% identical to the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642;

D6
wherein % identity is determined using the [Bestfit] Bestfit[®] program with parameters that calculate % identity over the full length of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of amino acid residues of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

Sub G7
127. An isolated polynucleotide comprising a first polynucleotide which hybridizes to a second polynucleotide, wherein the second polynucleotide consists [consisting] of the nucleotide sequence of the coding region of SEQ ID NO:41, or the full-length complement thereof, under conditions comprising:

D7
(a) incubating overnight at 42°C in a solution consisting of 50% formamide, 5x SSC, 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA; and

(b) washing at 65°C in a solution consisting of 0.1x SSC;
wherein said first polynucleotide is at least 70 nucleotides in length.